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Meta-analysis of incomplete Microarray Studies: Supplementary Materials

ALIX LEBOUCQ*, ANTHONY C. DAVISON, DARLENE R. GOLDSTEIN

EPFL SB MATHAA STAT, Station 8, 1015 Lausanne

alix.leboucq@epfl.ch

Summary

Meta-analysis of microarray studies to produce an overall gene list is relatively straightforward when complete data are available. When some studies lack information, for example, having only a ranked list of genes instead of complete primary data, it is common to reduce all studies to ranked lists prior to combining them. Since this entails a loss of information, we consider, in the main article, a hierarchical Bayes modeling approach to combine studies using the type of information available in each study: the full data matrix, summary statistics, or ranks for each gene. The model uses an informative prior for the parameter of interest, which eases the detection of differentially expressed genes.

Key words: Bayesian hierarchical model; Gibbs sampler; Horseshoe prior; Microarray; Normal-gamma prior; Serous ovarian cancer; Spike and slab prior.

*To whom correspondence should be addressed.

1. Introduction

This additional file is the Supplementary Materials for the article *Meta-analysis of Incomplete Microarray Studies*. We give here some additional figures and tables that illustrate the model developed in the paper, justify some of the choices that we made in the simulations or give some more information about the results in Section 2. We also give the detailed calculations for the posterior distributions for each parameter of the model in Section 3.

2. Figures and Tables

The hierarchical Bayesian model introduced in the main article, and represented as a directed acyclic graph in Figure 1, could choose from three priors for the parameter of interest γ. For each of these priors, Figures 2, 3 and 4 present a graphical representation of the corresponding hierarchical model, for the spike and slab (Mitchell and Beauchamp, 1988), the horseshoe (Carvalho *and others*, 2010) and the normal gamma priors (Griffin and Brown, 2010). A plot of the distribution of the parameter γ and some additional plots presenting the distribution of the variance of the parameter γ for the spike and slab and the normal gamma priors, or the parameter $\kappa_g = (1+\lambda_g^2)^{-1}$ for the horseshoe prior are also shown.

2.1 *Simulations and real data supplementary figures and tables*

In the simulation studies, we chose to discard some of the early iterations and perform thinning to reduce correlations between the draws. Figure 5 shows several diagnostic plots for the parameter γ, before and after adjusting for convergence and correlation. Each time, 31500 iterations were performed. Data were simulated using the simulation design presented in the article for a=0.5, $p = 200$ genes and $N = 50$ individuals. Two Type 1 studies and one study of each of the other types were generated according to this design. The model was fitted with the spike and slab prior. Based on these plots, we chose to discard the 1500 first draws to ensure convergence

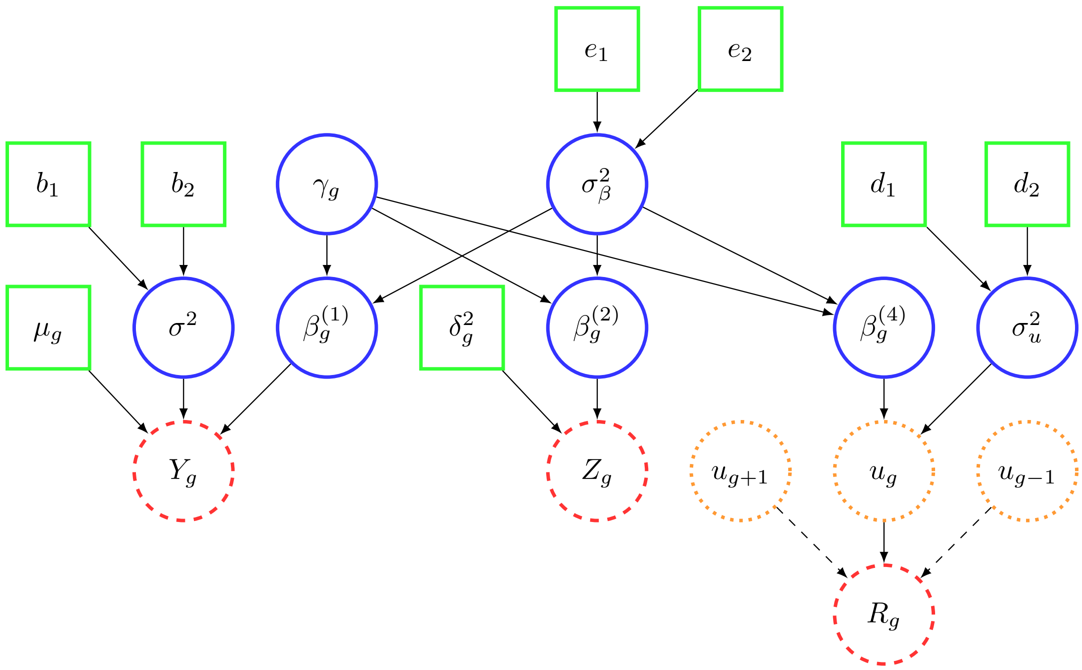


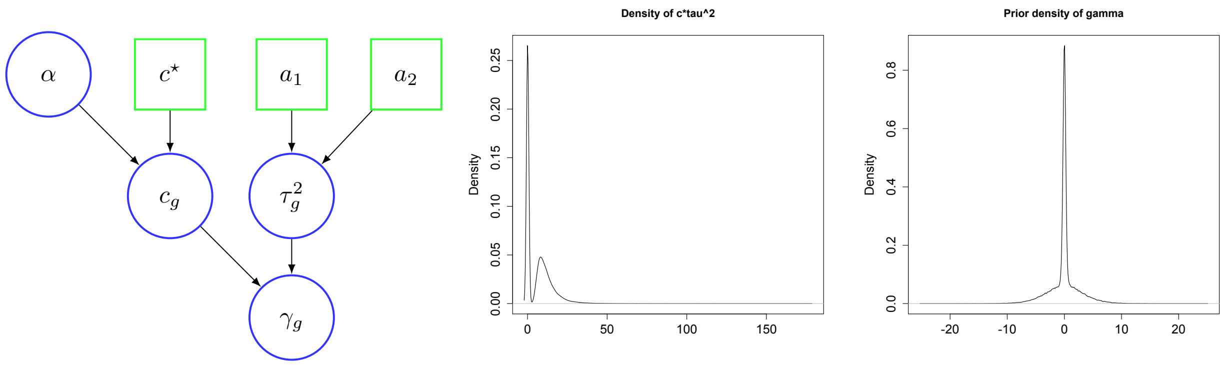
Fig. 1. Directed acyclic graph for the hierarchical model for one study per type. Type 3 studies are omitted as they are modeled and represented in the same way as Type 2 studies. Red dashed circles are data; among which Y denotes a full data matrix, Z a z-score and R a list of ranks. The variable u, in the orange dotted circle, is latent. Blue circles represent parameters, while green squares denote hyperparameters.

and to use a thinning of 10 to reduce correlation between the draws. Therefore we obtain 3000 quasi-independent draws for each parameter.

Table 1, gives the results of the formal test comparing the area under the curve (AUC) of two ROC curves corresponding to the combination of all studies and combination of full studies only, for different values of the parameter of differential expression a. All tests show that the difference is highly significant, suggesting that integrating all possible information leads to a clear power gain compared to only combining studies providing full information.

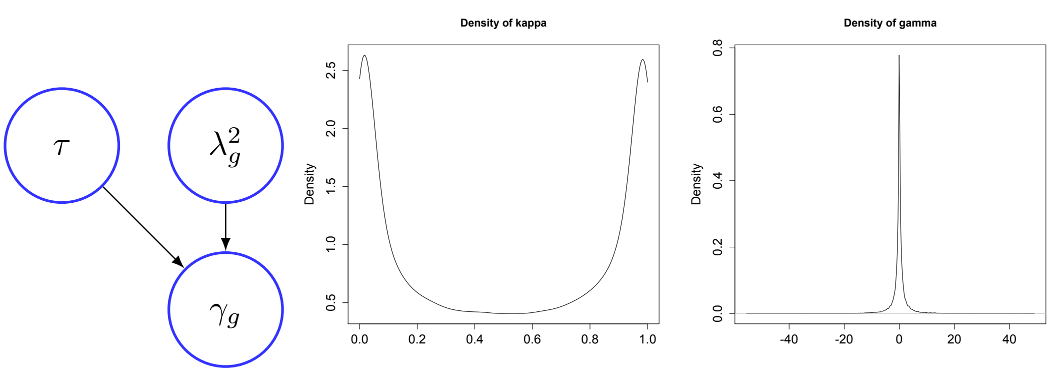
Figure 6 presents the posterior mean of w, the weight associated to each gene in the real data example, and used to discriminate differentially expressed and non differentially expressed genes. Recall that we call a gene significant if its corresponding weight is larger than 0.5. In

Fig. 2. The spike and slab prior. (a): Directed acyclic graph. Blue circles represent parameters, while green squares are hyperparameters. (b): Density of the variance of γ for the spike and slab prior. (c): Density of the mean parameter γ for the spike and slab prior.



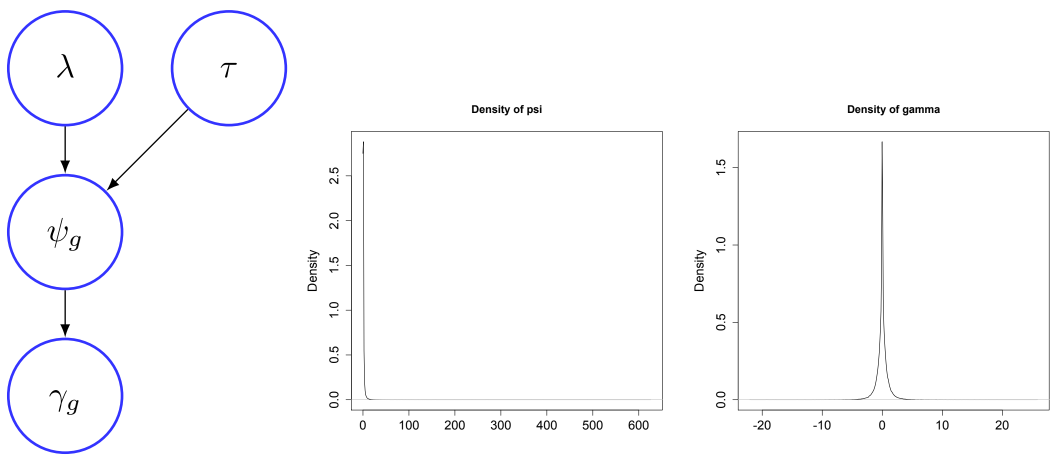
(a) Graphical model (b) Density of $c_g\tau_g^2$ (c) Density of γ

Fig. 3. The horseshoe prior. (a) Directed acyclic graph. (b): Density of the parameter κ.(c) Density of the mean parameter γ



(a) Graphical model (b) Density of κ_g (c) Density of γ

Fig. 4. The normal-gamma prior. (a): directed acyclic graph for the normal-gamma prior for γ. (b): density of the variance of of γ_g under the normal-gamma prior. (c): density of the mean parameter γ under the normal-gamma prior.

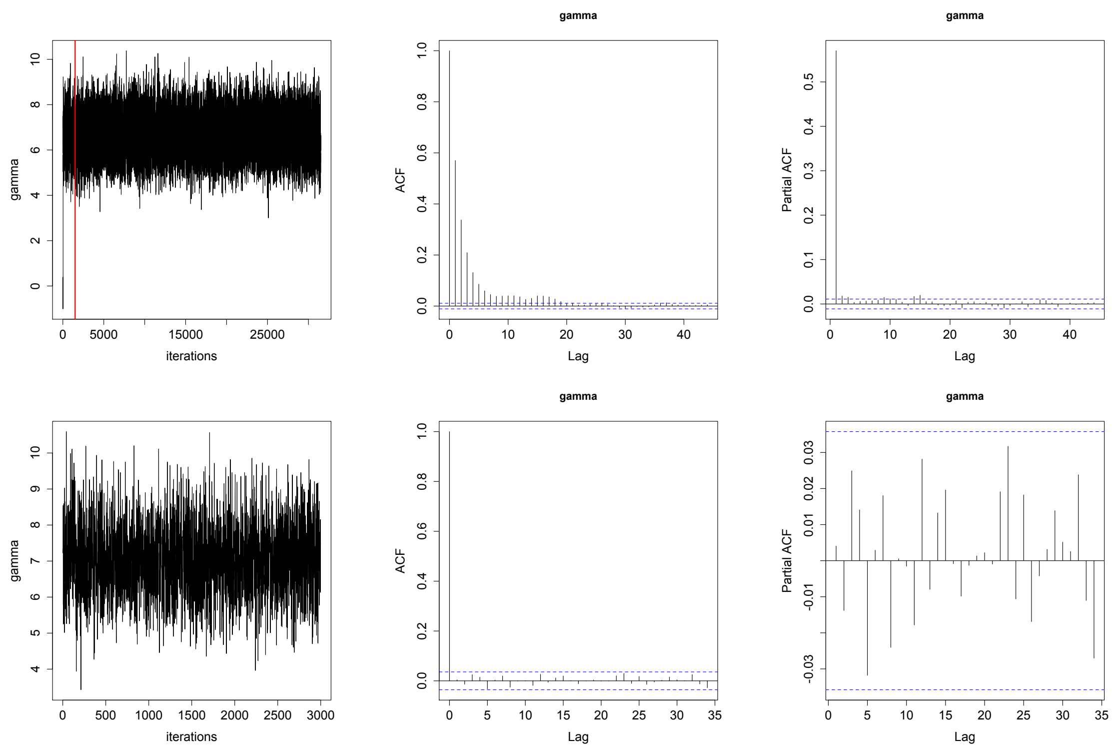


(a) Graphical model (b) Density of ψ_g (c) Density of γ_g

Table 1. AUC Comparison. Tests for comparing the areas under some ROC curves for different values of the parameter a using test from DeLong *and others* (1988).

		AUC	Z	p-value
a=0.2	design 1	0.539	-13.23	$< 2.2.10^{-16}$
	design 6	0.623		
a=0.3	design1	0.59	-26.36	$< 2.2.10^{-16}$
	design 6	0.75		
a=0.4	design 1	0.64	-33.97	$< 2.2.10^{-16}$
	design 6	0.84		
a=0.5	design 1	0.71	-32.97	$< 2.2.10^{-16}$
	design 6	0.90		
a=1	design 1	0.92	-22.28	$< 2.2.10^{-16}$
	design 6	0.98		

Fig. 5. Diagnostic plots (trace plot, ACF and PACF) for one parameter γ in one of the simulations, with $a = 0.5$ for the spike and slab prior. *First row:* 31500 iterations were performed without any thinning or warmup. *Second row*: 31500 iterations are performed with a warmup of 1500 and a thinning of 10.



this example, 296 genes fulfilled this criterion, and the values of the corresponding $\widehat{w}$ and $\widehat{\gamma}$ are presented in Tables 2, 3 and 4.

3. Computation of the posterior densities

In this section, we present the details of the calculations needed to obtain the posterior densities of the model parameters. We suppose we have L_i studies of type i. For simplicity, exponents indicating the study or its type will be omitted in the calculations when not necessary. In what follows, $\pi(\cdot)$ denotes prior densities, whereas, $\pi(\cdot \mid \cdot)$ denotes the posterior.

Table 2. List of the top 100 differentially expressed genes. Genes are ordered according to the value of $\widehat{w}$, from the most to the least differentially expressed genes. The estimates $\widehat{w}$ are obtained from the fit of our model to the 11 studies selected for the analysis, $\widehat{\gamma}$ gives indication about the magnitude and the direction of the differential expression. Genes in bold are known to be involved in ovarian cancer.

Rank	Genes	$\widehat{w}$	sd($\widehat{w}$)	$\widehat{\gamma}$	sd($\widehat{\gamma}$)
1	CP	0.99	$< 10^{-2}$	3.07	0.38
2	**TOP2A**	0.99	$< 10^{-2}$	2.60	0.38
3	BCHE	0.99	0.01	-2.49	0.41
4	NEK2	0.99	0.01	2.48	0.38
5	TTK	0.99	0.01	2.48	0.38
6	CENPA	0.99	0.02	2.45	0.38
7	SPP1	0.99	0.02	2.31	0.39
8	**MELK**	0.99	0.02	2.35	0.39
9	PRAME	0.99	0.02	2.41	0.39
10	ADH1B	0.99	0.02	-2.33	0.41
11	KIAA0101	0.99	0.02	2.41	0.40
12	NMU	0.99	0.02	2.30	0.39
13	IGFBP6	0.99	0.03	-2.22	0.39
14	**KLK6**	0.99	0.02	2.24	0.39
15	EVI1	0.99	0.01	2.67	0.45
16	**CLDN3**	0.99	0.02	2.38	0.41
17	SST	0.99	0.02	2.27	0.41
18	FOLR1	0.99	0.03	2.22	0.39
19	**WFDC2**	0.99	0.03	2.30	0.40
20	UBE2C	0.99	0.03	2.22	0.38
21	CD24	0.99	0.03	2.47	0.45
22	HMGA2	0.99	0.04	2.21	0.43
23	SPARCL1	0.99	0.04	-2.00	0.38
24	KIF2C	0.99	0.04	2.08	0.40
25	ELF3	0.99	0.05	2.11	0.41
26	**MAL**	0.99	0.05	2.07	0.42
27	CDKN2A	0.98	0.05	2.09	0.41
28	**PAX8**	0.98	0.05	2.05	0.41
29	FOXM1	0.98	0.05	2.05	0.40
30	CENPF	0.98	0.06	2.02	0.40
31	TNNT1	0.98	0.06	2.01	0.42
32	**CLDN4**	0.98	0.06	2.05	0.42
33	HMMR	0.98	0.07	1.99	0.42
34	LCT	0.98	0.07	1.94	0.41
35	KIF11	0.98	0.07	1.92	0.41
36	TRIM31	0.98	0.08	1.92	0.43
37	CDC20	0.98	0.08	1.88	0.42
38	**TACSTD1**	0.98	0.08	2.61	0.63
39	**CCNB1**	0.97	0.09	1.87	0.44
40	PTTG1	0.97	0.10	1.93	0.48
41	PRSS8	0.97	0.10	1.87	0.46
42	CCNE1	0.97	0.11	1.80	0.45
43	RRM2	0.96	0.11	1.84	0.47
44	EHF	0.96	0.11	1.90	0.48
45	**S100A1**	0.96	0.11	1.82	0.47
46	ATP6V1B1	0.95	0.13	1.75	0.50
47	KLK7	0.95	0.13	1.72	0.48
48	ABCA8	0.95	0.13	-1.77	0.49
49	ALDH1A1	0.95	0.13	-1.70	0.47
50	SCNN1A	0.94	0.14	1.73	0.51

Rank	Genes	$\widehat{w}$	sd($\widehat{w}$)	$\widehat{\gamma}$	sd($\widehat{\gamma}$)
51	C7	0.94	0.14	-1.69	0.52
52	PDHA2	0.94	0.15	1.70	0.52
53	ANXA8	0.94	0.17	2.22	0.74
54	GLDC	0.94	0.15	1.66	0.49
55	LAMP3	0.94	0.16	1.72	0.54
56	KRT7	0.93	0.16	1.57	0.50
57	CKS2	0.93	0.16	1.61	0.50
58	AOX1	0.93	0.16	-1.63	0.53
59	EZH2	0.93	0.16	1.60	0.49
60	MYH11	0.93	0.16	-1.63	0.51
61	NY-REN-7	0.92	0.20	2.41	0.94
62	CCNA2	0.91	0.18	1.51	0.53
63	TK1	0.91	0.18	1.50	0.52
64	MAD2L1	0.91	0.18	1.51	0.54
65	ACTG2	0.91	0.18	-1.53	0.56
66	SCGB2A1	0.91	0.19	1.65	0.64
67	**MUC1**	0.90	0.19	1.52	0.57
68	SLC2A1	0.90	0.19	1.46	0.53
69	SULT1C2	0.89	0.20	1.47	0.57
70	MGP	0.87	0.21	-1.37	0.55
71	THBD	0.87	0.21	-1.38	0.57
72	IGF2BP3	0.86	0.22	1.36	0.58
73	SPINT2	0.86	0.22	1.36	0.58
74	ZIC1	0.86	0.22	1.38	0.60
75	CGN	0.85	0.24	1.44	0.66
76	RNASE4	0.85	0.22	-1.31	0.57
77	EFEMP1	0.85	0.22	-1.33	0.60
78	APOA1	0.85	0.23	1.31	0.59
79	DXYS155E	0.84	0.28	2.22	1.21
80	TFAP2A	0.83	0.23	1.25	0.57
81	NDP52	0.83	0.29	2.21	1.27
82	FRY	0.82	0.24	-1.25	0.62
83	DEFB1	0.79	0.25	1.12	0.59
84	TYMS	0.79	0.25	1.12	0.56
85	GRPR	0.79	0.25	1.15	0.60
86	MYBL2	0.79	0.25	1.13	0.58
87	MAOB	0.79	0.25	-1.11	0.56
88	CNN1	0.77	0.25	-1.08	0.57
89	CLDN7	0.77	0.26	1.14	0.64
90	BLM	0.77	0.25	1.09	0.59
91	CXCL10	0.76	0.25	1.07	0.61
92	KIF23	0.76	0.25	1.04	0.56
93	KLF4	0.76	0.25	-1.03	0.56
94	CDKN3	0.75	0.26	1.03	0.57
95	HTR3A	0.75	0.25	1.02	0.57
96	EPCAM	0.75	0.27	1.09	0.67
97	GNG11	0.75	0.26	-1.01	0.55
98	KIF14	0.74	0.25	1.00	0.55
99	NDN	0.74	0.25	-0.99	0.54
100	RAD54L	0.74	0.25	0.98	0.55

Table 3. List of top 101-200 differentially expressed genes. Genes are ordered according to the value of $\widehat{w}$, from the most to the least differentially expressed genes. The estimates $\widehat{w}$ are obtained from the fit of our model to the 11 studies selected for the analysis.

Rank	Genes	$\widehat{w}$	sd($\widehat{w}$)	$\widehat{\gamma}$	sd($\widehat{\gamma}$)
101	CBS	0.74	0.26	0.99	0.57
102	TROAP	0.74	0.25	0.96	0.55
103	FXYD3	0.74	0.26	1.01	0.60
104	DKFZP586A0522	0.74	0.33	1.60	1.14
105	KIAA1536	0.72	0.33	1.52	1.14
106	GPR19	0.72	0.26	0.93	0.55
107	SE20-4	0.72	0.33	1.65	1.28
108	SFN	0.71	0.26	0.92	0.55
109	ISG15	0.70	0.26	0.91	0.58
110	SLC6A6	0.70	0.26	0.91	0.57
111	MAS1	0.70	0.26	0.90	0.56
112	KRT2	0.70	0.26	0.89	0.55
113	ESPL1	0.70	0.26	0.89	0.53
114	CDH6	0.69	0.26	0.89	0.58
115	SLPI	0.69	0.26	0.86	0.57
116	TRIP13	0.68	0.25	0.83	0.52
117	DCN	0.67	0.27	-0.87	0.57
118	RXRG	0.66	0.25	0.78	0.51
119	GRM8	0.66	0.25	0.79	0.50
120	MTHFD2	0.66	0.25	0.78	0.51
121	FLJ13236	0.66	0.32	1.09	0.86
122	SPINT1	0.65	0.27	0.83	0.58
123	UCP2	0.65	0.25	0.76	0.52
124	TACSTD2	0.65	0.25	0.76	0.55
125	DES	0.65	0.25	-0.74	0.51
126	MAGEA1	0.64	0.25	0.75	0.50
127	MCM4	0.64	0.25	0.75	0.49
128	LMNB1	0.64	0.25	0.76	0.52
129	GIF	0.64	0.25	0.75	0.50
130	CPT1B	0.64	0.30	0.93	0.76
131	TACR3	0.64	0.25	0.73	0.48
132	LAD1	0.64	0.25	0.74	0.50
133	LCN2	0.63	0.25	0.71	0.49
134	ETV4	0.62	0.25	0.69	0.48
135	DLC1	0.62	0.26	-0.73	0.55
136	MAOA	0.62	0.24	-0.68	0.48
137	AQP5	0.62	0.24	0.68	0.48
138	S100A8	0.61	0.24	-0.67	0.50
139	CAV1	0.61	0.24	-0.68	0.46
140	GCG	0.61	0.24	0.66	0.43
141	HOXB1	0.61	0.24	0.66	0.48
142	CDC25C	0.60	0.24	0.66	0.47
143	HNF4A	0.60	0.24	0.65	0.45
144	MMP13	0.60	0.24	0.64	0.46
145	PLK1	0.60	0.24	0.65	0.44
146	PTGIS	0.60	0.25	-0.66	0.50
147	DHCR24	0.60	0.24	0.65	0.44
148	KIFC1	0.60	0.24	0.64	0.44
149	SOX17	0.60	0.26	0.69	0.55
150	C4A	0.60	0.34	1.06	1.01

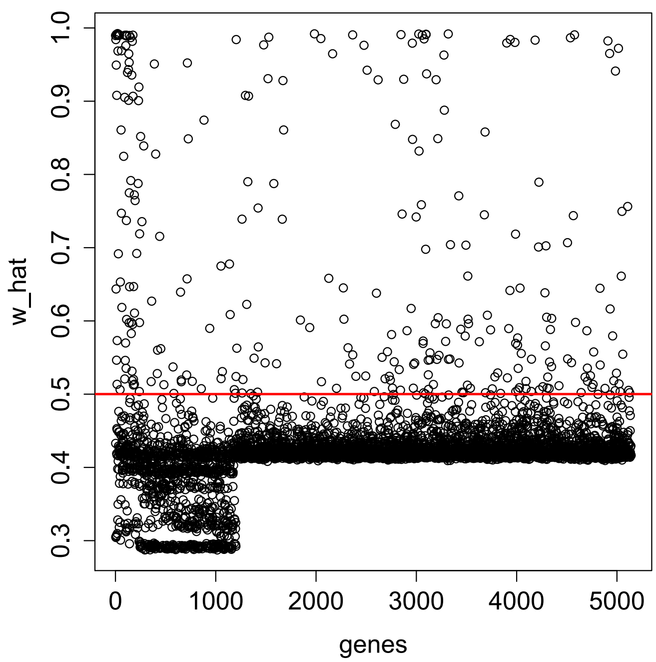
Rank	Genes	$\widehat{w}$	sd($\widehat{w}$)	$\widehat{\gamma}$	sd($\widehat{\gamma}$)
151	DUSP1	0.60	0.24	-0.63	0.49
152	EPHA1	0.60	0.24	0.63	0.44
153	SPRR1B	0.60	0.24	0.64	0.44
154	CFD	0.60	0.24	-0.64	0.43
155	ID3	0.60	0.24	-0.63	0.49
156	CDH1	0.59	0.24	0.63	0.45
157	FHL1	0.59	0.23	-0.61	0.43
158	PHOX2B	0.59	0.23	0.61	0.43
159	BIK	0.59	0.23	0.61	0.44
160	GLP1R	0.59	0.23	0.63	0.45
161	GABRR1	0.59	0.23	0.61	0.43
162	MMP7	0.59	0.24	0.62	0.47
163	WNT7A	0.59	0.23	0.60	0.44
164	HIST1H2BG	0.58	0.28	0.69	0.59
165	LMOD1	0.58	0.23	-0.59	0.43
166	MYCL1	0.58	0.23	0.59	0.43
167	PNOC	0.58	0.23	0.59	0.45
168	SLC15A1	0.58	0.23	0.59	0.43
169	SCGB1D2	0.57	0.26	0.61	0.57
170	DSC2	0.57	0.23	0.58	0.41
171	PLAG1	0.57	0.23	0.58	0.43
172	CR1	0.57	0.22	0.58	0.41
173	ALDH1A3	0.57	0.23	-0.57	0.46
174	SLC10A1	0.57	0.23	0.58	0.41
175	NAP1L3	0.57	0.22	-0.58	0.42
176	MEP1B	0.57	0.22	0.57	0.40
177	IL9	0.57	0.22	0.57	0.42
178	CDC25A	0.56	0.22	0.57	0.42
179	SPOCK1	0.56	0.22	-0.55	0.41
180	CYP2A6	0.56	0.22	0.56	0.41
181	FLJ14957	0.56	0.34	0.98	1.05
182	MCM2	0.56	0.22	0.55	0.40
183	PROCR	0.56	0.22	-0.55	0.41
184	COL19A1	0.56	0.22	0.54	0.41
185	ALDH3B2	0.56	0.22	0.55	0.39
186	HTR1D	0.56	0.21	0.54	0.39
187	RUNX2	0.55	0.22	0.54	0.40
188	TRIM29	0.55	0.22	0.53	0.42
189	PLS1	0.55	0.22	0.53	0.40
190	RTN1	0.55	0.21	-0.53	0.39
191	MCF2	0.55	0.22	0.52	0.39
192	NR2F6	0.55	0.22	0.52	0.38
193	CCL20	0.55	0.21	0.52	0.40
194	CACNB4	0.55	0.21	0.51	0.38
195	NPY1R	0.55	0.21	-0.53	0.40
196	LAMA2	0.55	0.21	-0.52	0.38
197	PLN	0.55	0.21	-0.52	0.38
198	IDH2	0.55	0.22	0.51	0.40
199	MSLN	0.55	0.21	0.52	0.39
200	RGS1	0.55	0.22	0.52	0.45

Table 4. List of top 201-296 differentially expressed genes. Genes are ordered according to the value of $\widehat{w}$, from the most to the least differentially expressed genes. The estimates $\widehat{w}$ are obtained from the fit of our model to the 11 studies selected for the analysis.

Rank	Genes	$\widehat{w}$	sd($\widehat{w}$)	$\widehat{\gamma}$	sd($\widehat{\gamma}$)
201	KIF1A	0.54	0.21	0.51	0.40
202	PCDH11X	0.54	0.21	0.52	0.38
203	GPM6A	0.54	0.21	-0.51	0.37
204	SIM2	0.54	0.21	0.50	0.40
205	TNNI3	0.54	0.21	0.51	0.38
206	CDC7	0.54	0.21	0.52	0.39
207	ERBB3	0.54	0.21	0.51	0.38
208	IFI27	0.54	0.21	0.51	0.40
209	MMP1	0.54	0.21	0.50	0.39
210	SDC2	0.54	0.21	-0.50	0.37
211	ELAVL2	0.54	0.21	0.50	0.38
212	EFG1	0.54	0.33	0.94	1.07
213	MPZ	0.54	0.20	0.50	0.38
214	CXCR4	0.54	0.21	0.48	0.41
215	DEFA4	0.54	0.21	0.50	0.37
216	RFC4	0.53	0.21	0.49	0.38
217	BMP2	0.53	0.20	-0.47	0.36
218	KLF2	0.53	0.22	-0.53	0.39
219	ZNF165	0.53	0.20	0.48	0.36
220	IFNA5	0.53	0.20	0.48	0.36
221	LOC286286	0.53	0.33	0.85	0.98
222	PLK4	0.53	0.20	0.47	0.35
223	ST14	0.53	0.20	0.46	0.35
224	CASR	0.53	0.20	0.46	0.37
225	HK2	0.52	0.20	0.46	0.37
226	EPS8	0.52	0.20	-0.47	0.36
227	E2F3	0.52	0.20	0.46	0.36
228	DDR1	0.52	0.20	0.46	0.36
229	SLC5A1	0.52	0.20	0.46	0.35
230	PGR	0.52	0.19	-0.46	0.35
231	CXCL11	0.52	0.21	0.46	0.37
232	PTH	0.52	0.20	0.45	0.35
233	AP1M2	0.52	0.22	0.49	0.39
234	GGH	0.52	0.20	0.46	0.35
235	NPPB	0.52	0.21	0.45	0.40
236	BAMBI	0.52	0.20	-0.46	0.36
237	SMPDL3B	0.52	0.20	0.47	0.35
238	TYRP1	0.52	0.20	0.45	0.34
239	EMP3	0.52	0.19	-0.46	0.32
240	DFNA5	0.52	0.22	-0.49	0.41
241	BCAT1	0.52	0.20	0.45	0.36
242	XDH	0.52	0.19	0.44	0.34
243	HIST1H1C	0.52	0.19	0.44	0.34
244	GNAT1	0.52	0.19	0.45	0.33
245	KIAA0222	0.52	0.32	0.82	0.95
246	APOD	0.52	0.20	-0.47	0.34
247	MAL2	0.52	0.24	0.54	0.46
248	FRMPD4	0.51	0.19	0.44	0.33

Rank	Genes	$\widehat{w}$	sd($\widehat{w}$)	$\widehat{\gamma}$	sd($\widehat{\gamma}$)
249	CRABP1	0.51	0.19	0.42	0.35
250	CHI3L1	0.51	0.22	0.48	0.45
251	COL4A6	0.51	0.19	-0.44	0.34
252	RAD51	0.51	0.19	0.46	0.35
253	SOX9	0.51	0.19	0.43	0.33
254	KRT23	0.51	0.22	0.48	0.41
255	TDO2	0.51	0.19	0.44	0.34
256	MCM7	0.51	0.19	0.43	0.32
257	TACR1	0.51	0.19	0.44	0.33
258	GRB7	0.51	0.19	0.42	0.32
259	HTR2C	0.51	0.19	0.43	0.32
260	AVPR1B	0.51	0.19	0.44	0.32
261	CD302	0.51	0.19	-0.43	0.32
262	GEM	0.51	0.19	-0.43	0.34
263	ANKRD1	0.51	0.18	0.42	0.32
264	MEST	0.51	0.19	0.42	0.33
265	MFAP4	0.51	0.19	-0.43	0.33
266	UGT8	0.51	0.19	0.42	0.35
267	CHRNB4	0.51	0.18	0.43	0.31
268	KRT19	0.51	0.23	0.52	0.44
269	CDKL5	0.51	0.19	0.43	0.32
270	AOC3	0.51	0.19	-0.42	0.34
271	NBEA	0.51	0.21	-0.47	0.36
272	KLK10	0.51	0.21	0.44	0.39
273	CSN2	0.51	0.18	0.42	0.31
274	APOF	0.51	0.19	0.42	0.34
275	PRKX	0.51	0.18	0.42	0.30
276	CHRM5	0.51	0.19	0.42	0.32
277	ABO	0.50	0.18	0.42	0.33
278	PAX3	0.50	0.18	0.41	0.33
279	PAFAH1B3	0.50	0.19	0.42	0.32
280	ARHI	0.50	0.32	0.78	0.95
281	JAK3	0.50	0.18	0.42	0.31
282	EPHA5	0.50	0.18	0.43	0.31
283	SIX1	0.50	0.19	0.39	0.33
284	CXADR	0.50	0.18	0.40	0.33
285	ITGB8	0.50	0.18	0.41	0.32
286	NPPA	0.50	0.18	0.39	0.33
287	MC4R	0.50	0.19	0.40	0.32
288	PRSS1	0.50	0.18	0.41	0.32
289	SCGB2A2	0.50	0.19	0.42	0.33
290	GNAO1	0.50	0.18	0.41	0.30
291	NT5E	0.50	0.18	-0.40	0.32
292	PRKCI	0.50	0.18	0.41	0.31
293	EDN2	0.50	0.18	0.41	0.31
294	E2F1	0.50	0.18	0.41	0.32
295	RAG1	0.50	0.19	0.41	0.33
296	CKM	0.50	0.18	0.41	0.32

Fig. 6. Estimates of w for all genes included in the analysis. The 1 200 first genes correspond to genes present in the union of all partial studies (Types 3 and 4), whereas the remaining genes were selected from the intersection of all genes in the full studies (Types 1 and 2). Genes with corresponding $\widehat{w} > 0.5$ are considered differentially expressed.



3.1 *Realisations of* $\pi\left(\beta_g^{(1)} \mid rest\right)$.

$$
\begin{aligned}
\pi\left(\beta_g^{(1)} \mid \text{rest}\right) &\propto \exp\left\{\frac{-(\beta_g-\gamma_g)^2}{2\sigma_\beta^2}\right\}\prod_{j=1}^{n_1}\exp\left\{\frac{-(y_{gj}-(\beta_g+\mu_g))^2}{2\sigma_g^2}\right\}\prod_{j=n_1+1}^{N}\exp\left\{\frac{-(y_{gj}-\mu_g)^2}{2\sigma_g^2}\right\}\\
&\propto \exp\left\{\frac{-\beta_g^2\sigma_g^2+2\beta_g\gamma_g\sigma_g^2-\gamma_g^2\sigma_g^2-\sum_{j=1}^{n_1}y_{gj}^2\sigma_\beta^2+2(\beta_g+\mu_g)\sigma_\beta^2\sum_{i=1}^{n_1}y_{gj}}{2\sigma_\beta^2\sigma_g^2}\right.\\
&\qquad\left.-\frac{n_1(\beta_g+\mu_g)^2\sigma_\beta^2}{2\sigma_\beta^2\sigma_g^2}\right\}\\
&\propto \exp\left\{\frac{-\beta_g^2[\sigma_g^2+n_1\sigma_\beta^2]+2\beta_g[\gamma_g\sigma_g^2+\sigma_\beta^2\sum_{j=1}^{n_1}y_{gj}-n_1\sigma_\beta^2\mu_g]}{2\sigma_g^2\sigma_\beta^2}\right\}\\
&\sim \mathcal{N}\left(\frac{\gamma_g\sigma_g^2+\sigma_\beta^2\sum_{j=1}^{n_1}y_{gj}-n_1\sigma_\beta^2\mu_g}{\sigma_g^2+n_1\sigma_\beta^2},\frac{\sigma_\beta^2\sigma_g^2}{\sigma_g^2+n_1\sigma_\beta^2}\right).
\end{aligned}
$$

3.2 *Realisations of* $\pi\left(\sigma_g^{-2} \mid rest\right)$.

$$
\begin{aligned}
\pi(\sigma^{-2} \mid \text{rest}) &\propto \prod_{j=1}^{N} \pi(Y_{gj} \mid \mu_g, \beta_g, \sigma_g^{-2}) \pi(\sigma^{-2} \mid b, h) \\
&\propto (\sigma_g^{-2})^{b-1} \exp\left\{-\sigma_g^{-2} h\right\} \exp\left\{\frac{-\sum_{j=1}^{n_1} (Y_{gj} - \mu_g - \beta_g)^2 \sigma_g^{-2}}{2}\right\} \\
&\exp\left\{\frac{-\sum_{g=n_1+1}^{n} (Y_{gj} - \mu_g)^2 \sigma_g^{-2}}{2}\right\} \left(\sigma^{-2}\right)^{\frac{N}{2}} \\
&\sim \text{Gamma}\left(b + \frac{N}{2}, h + \frac{1}{2}\sum_{j=1}^{n_1} (Y_{gj} - \mu_g - \beta_g)^2 + \frac{1}{2}\sum_{j=n_1+1}^{n} (Y_{gj} - \mu_g)^2\right).
\end{aligned}
$$

3.3 *Realisations of* $\pi\left(\beta_g^{(2)} \mid rest\right)$.

$$
\begin{aligned}
\pi\left(\beta_g^{(2)} \mid \text{rest}\right) &\propto \pi(\beta_g^{(2)} \mid \gamma_g, \sigma_\beta^2) \pi(z_g^{(2)} \mid \beta_g^{(2)}, \delta_g^2) \\
&\propto \exp\left\{\frac{-(\beta_g - \gamma_g)^2}{2\sigma_\beta^2}\right\} \exp\left\{\frac{-(z_g - \beta_g\sqrt{\delta_g^2 \nu})^2}{2}\right\} \\
&\propto \exp\left\{\frac{-\beta_g^2 + 2\beta_g\gamma_g - \gamma_g^2 - z_g^2\sigma_\beta^2 + 2z_g\beta_g\sigma_\beta^2\sqrt{\delta_g^2\nu} - \beta_g^2\sigma_\beta^2\delta_g^2\nu}{2\sigma_\beta^2}\right\} \\
&\propto \exp\left\{\frac{-\beta_g^2(1 + \delta_g^2\nu\sigma_\beta^2) + 2\beta_g(\gamma_g + z_g\sigma_\beta^2\sqrt{\delta_g^2\nu})}{2\sigma_\beta^2}\right\} \\
&\sim \mathcal{N}\left(\frac{\gamma_g + z_g\sigma_\beta^2\sqrt{\delta_g^2\nu}}{1 + \delta_g^2\nu\sigma_\beta^2}, \frac{\sigma_\beta^2}{1 + \delta_g^2\nu\sigma_\beta^2}\right).
\end{aligned}
$$

The calculations are the same for $\beta_g^{(3)}$.

3.4 *Realisations of* $\pi\left(\beta_g^{(4)} \mid rest\right)$.

$$
\begin{aligned}
\pi(\beta_g^{(4)} \mid \text{rest}) &\propto \pi(\beta_g \mid \gamma_g, \sigma_\beta^2)\pi(u_g \mid \beta_g, \sigma_{u,g}^2) \\
&\propto \exp\left\{\frac{-(\beta_g - \gamma_g)^2}{2\sigma_\beta^2} - \frac{(u_g - \beta_g\sqrt{\nu})^2}{2\sigma_{u,g}^2}\right\} \\
&\propto \exp\left\{\frac{-\beta_g^2(\sigma_{u,g}^2 + \sigma_\beta^2\nu) + 2\beta_g(\gamma_g\sigma_{u,g}^2 + u_g\sigma_\beta^2\sqrt{\nu})}{2\sigma_\beta^2\sigma_{u,g}^2}\right\} \\
&\sim \mathcal{N}\left(\frac{\gamma_g\sigma_{u,g}^2 + u_g\sigma_\beta^2\sqrt{\nu}}{\sigma_{u,g}^2 + \nu\sigma_\beta^2}, \frac{\sigma_\beta^2\sigma_{u,g}^2}{\sigma_{u,g}^2 + \sigma_\beta^2\nu}\right).
\end{aligned}
$$

3.5 *Realisations of* $\pi\left(u_g \mid rest\right)$.

$$
\begin{aligned}
\pi(u_g \mid \text{rest}) &\propto \pi(R_g \mid u_{g-1}, u_g, u_{g+1})\pi(u_g \mid \beta_g^{(4)}, \sigma_{u,g}^2) \\
&\propto I_{\{|u_{g+1}|<|u_g|<|u_{g-1}|\}} \exp\left\{\frac{-(u_g - \beta_g\sqrt{\nu})^2}{2\sigma_{u,g}^2}\right\} \\
&\sim \mathcal{N}_{|u_{g+1}|}^{|u_{g-1}|}\left(\beta_g\sqrt{\nu}, \sigma_{u,g}^2\right),
\end{aligned}
$$

where $\mathcal{N}_b^a$ corresponds to a truncated normal between a and b. To generate from the truncated normal, we first center and scale the random variable u_g, and obtain

$$
Z_g = \frac{u_g - \beta_g^{(4)}\sqrt{\nu}}{\sigma_{u,g}}, \quad z^+ = \frac{u_{g-1} - \beta_g^{(4)}\sqrt{\nu}}{\sigma_{u,g}}, \quad z^- = \frac{u_{g+1} - \beta_g^{(4)}\sqrt{\nu}}{\sigma_{u,g}}.
$$

Then,

$$
\begin{aligned}
\alpha &= P(Z \leqslant z \mid z^- < z < z^+) \\
&= \frac{P(Z \leqslant z, z^- < z < z^+)}{P(z^- < z < z^+)} \\
&= \frac{P(z^- < Z < z)}{\Phi(z^+) - \Phi(z^-)} \\
&= \frac{\Phi(z) - \Phi(z^-)}{\Phi(z^+) - \Phi(z^-)}.
\end{aligned}
$$

Therefore, $z = \Phi^{-1}\left[\alpha\left\{\Phi(z^+) - \Phi(z^-)\right\} + \Phi(z^-)\right]$, and thus,

$$
u_g = \Phi^{-1}\left[\alpha\left\{\Phi(z^+) - \Phi(z^-)\right\} + \Phi(z^-)\right]\sigma_u + \beta_g^{(4)}\sqrt{\nu},
$$

where $\alpha \sim \mathcal{U}(0,1)$. The calculations here are for a positive u_g, the negative version being similar. As the sign of u is not observed and interest only lies in the expected value of this variable, we fix the sign of u_g to be the same that of the corresponding $\beta_g^{(4)}$.

3.6 *Realisations of* $\pi\left(\sigma_{u,g}^{-2} \mid rest\right)$.

$$\begin{aligned}\pi(\sigma_{u,g}^{-2} \mid \text{rest}) &\propto \pi(\sigma_{u,g}^{-2} \mid d_1, d_2)\pi(u_g \mid \beta_g, \sigma_{u,g}^{-2}) \\ &\sim \text{Gamma}\left(d_1 + \frac{1}{2}, d_2 + \frac{(u_g - \beta_g\sqrt{\nu})^2}{2}\right).\end{aligned}$$

3.7 *Realisations of* $\pi\left(\sigma_\beta^{-2} \mid rest\right)$.

$$\begin{aligned}\pi(\sigma_\beta^{-2} \mid \text{rest}) &\propto \pi(\sigma_\beta^{-2} \mid e_1, e_2)\prod_{g=1}^{p}\prod_{l=1}^{L}\pi(\beta_g^{(l)} \mid \gamma_g, \sigma_\beta^{-2}) \\ &\propto (\sigma_\beta^{-2})^{e_1-1}e^{-\sigma_\beta^{-2}e_2}\prod_{g=1}^{p}\prod_{l=1}^{L}\exp\left\{\frac{-(\beta_g^{(l)} - \gamma_g)^2\sigma_\beta^{-2}}{2}\right\}\left(\sqrt{\sigma_\beta^{-2}}\right)^{pL} \\ &\sim \text{Gamma}\left(e_1 + \frac{pL}{2}, e_2 + \sum_{g=1}^{p}\sum_{l=1}^{L}\frac{(\beta_g^{(l)} - \gamma_g)^2}{2}\right).\end{aligned}$$

3.8 *Posterior densities for the spike and slab prior.*

3.8.1 *Realisations of* $\pi\left(\alpha \mid rest\right)$

$$\begin{aligned}\pi(\alpha \mid \text{rest}) &\propto \pi(\alpha)\prod_{g=1}^{p}\pi(c_g \mid c^\star, \alpha) \\ &\propto \prod_{g=1}^{p}(1-\alpha)\delta_{c^\star} + \alpha\delta_1 \\ &\propto (1-\alpha)^{\#\{g:c_g=c^\star\}}\alpha^{\#\{g:c_g=1\}} \\ &\sim \text{Beta}\left(1 + \#\{g : c_g = 1\}, 1 + \#\{g : c_g = c^\star\}\right).\end{aligned}$$

3.8.2 *Realisations of* $\pi(c_g \mid rest)$

$$\begin{aligned}\pi(c_g \mid \text{rest}) &\propto \pi(c_g \mid c^\star, \alpha)\pi(\gamma_g \mid c_g) \\ &\propto \{(1-\alpha)\delta_{c^\star} + \alpha\delta_1\}\frac{1}{\sqrt{c_g}}\exp\left(\frac{-\gamma_g^2}{2c_g\tau_g^2}\right).\end{aligned}$$

We define the following quantities:

$$w_{1,g} = \frac{1-\alpha}{\sqrt{c^\star}}\exp\left(\frac{-\gamma_g^2}{2c^\star\tau_g^2}\right), \quad w_{2,g} = \alpha\exp\left(\frac{-\gamma_g^2}{2\tau_g^2}\right),$$

then,

$$c_g \mid \text{rest} \sim \frac{w_{1,g}}{w_{g,1} + w_{g,2}}\delta_{c^\star} + \frac{w_{2,g}}{w_{1,g} + w_{2,g}}\delta_1.$$

3.8.3 *Realisations of* $\pi(\tau_g^{-2} \mid rest)$

$$\begin{aligned}\pi(\tau_g^{-2} \mid \text{rest}) &\propto \pi(\tau_g^{-2} \mid a_1, a_2)\pi(\gamma_g \mid c_g, \tau_g^{-2}) \\ &\propto (\tau_g^{-2})^{a_1-1} e^{-\tau_g^{-2} a_2} \sqrt{\tau_g^{-2}} e^{-\frac{\gamma_g^2 \tau_g^{-2}}{2c_g}} \\ &\sim \text{Gamma}\left(a_1 + 1/2, a_2 + \frac{\gamma_g^2}{2c_g}\right).\end{aligned}$$

3.8.4 *Realisations of* $\pi(\gamma_g \mid rest)$

$$\begin{aligned}\pi\left(\gamma_g \mid \text{rest}\right) &\propto \pi(\gamma_g \mid c_g, \tau_g^2) \prod_{l=1}^{L} \pi\left(\beta_g^{(l)} \mid \gamma_g, \sigma_\beta^2\right) \\ &\propto \exp\left\{\frac{-\gamma_g^2}{2c_g\tau_g^2}\right\} \exp\left\{\frac{-\sum_{l=1}^{L}\left(\beta_g^{(l)} - \gamma_g\right)^2}{2\sigma_\beta^2}\right\} \\ &\propto \exp\left\{\frac{-\gamma_g^2\left(Lc_g\tau_g^2 + \sigma_\beta^2\right) + 2\gamma_g\left(\sum_{l=1}^{L}\beta_g^{(l)} c_g \tau_g^2\right)}{2\sigma_\beta^2 c_g \tau_g^2}\right\} \\ &\sim \mathcal{N}\left(\frac{\sum_{l=1}^{L}\beta_g^{(l)} c_g\tau_g^2}{Lc_g\tau_g^2 + \sigma_\beta^2}, \frac{\sigma_\beta^2 c_g \tau_g^2}{Lc_g\tau_g^2 + \sigma_\beta^2}\right).\end{aligned}$$

3.9 *Posterior densities for the horseshoe prior.*

3.9.1 *Realisations of* $\pi(\gamma_g \mid rest)$

$$\begin{aligned}\pi(\gamma_g \mid \text{rest}) &\propto \prod_{l=1}^{L} \pi(\beta_g^{(l)} \mid \gamma_g, \sigma_\beta^2)\pi(\gamma_g \mid \lambda_g^2, \tau^2) \\ &\propto \prod_{l=1}^{L} \exp\left\{\frac{-(\gamma_g - \beta_g^{(l)})^2}{2\sigma_\beta^2}\right\} \exp\left\{\frac{-\gamma_g^2}{2\lambda_g^2\tau^2}\right\} \\ &\propto \exp\left\{\frac{-\gamma_g^2(L\lambda_g^2\tau^2 + \sigma_\beta^2) + 2\gamma_g\sum_{l=1}^{L}\beta_g^{(l)}\lambda_g^2\tau^2}{2\sigma_\beta^2\lambda_g^2\tau^2}\right\} \\ &\sim \mathcal{N}\left(\frac{\sum_{l=1}^{L}\beta_g^{(l)}\lambda_g^2\tau^2}{L\lambda_g^2\tau^2 + \sigma_\beta^2}, \frac{\sigma_\beta^2\lambda_g^2\tau^2}{\sigma_\beta^2 + L\lambda_g^2\tau^2}\right).\end{aligned}$$

3.9.2 *Realisations of* $\pi(\lambda_g \mid rest)$

$$\begin{aligned}\pi(\lambda_g \mid \text{rest}) &\propto \pi(\gamma_g \mid \lambda_g, \tau)\pi(\lambda_g) \\ &\propto \frac{1}{\lambda_g\tau} \exp\left\{\frac{-\gamma_g^2}{2\lambda_g^2\tau^2}\right\} \frac{1}{1+\lambda_g^2}.\end{aligned}$$

It seems difficult to sample from this posterior distribution. Therefore, we follow the algorithm described in Scott (2011), which was adapted from the method described in Damien (1999). We first define

$$\eta_g = \frac{1}{\lambda_g^2}, \quad \varphi_g = \frac{\gamma_g}{\tau}.$$

We can now compute the posterior distribution of η_g,

$$\pi(\eta_g \mid \varphi_g) \propto \exp\left(\frac{-\varphi_g^2 \eta_g}{2}\right) \frac{1}{1+\eta_g}.$$

Then the algorithm is

- Sample $u_g \sim \mathcal{U}(0, 1/(1+\eta_g))$.
- Generate $\eta_g \sim E(\varphi_g^2/2)$, truncated to have 0 probability outside the interval $\left[0, \frac{1-u_g}{u_g}\right]$.
- Transform back to the λ-scale to obtain a sample from the desired posterior distribution: $\lambda_g = \sqrt{1/\eta_g}$.

In order to sample from a truncated exponential distribution, we first denote $u^+ = (1-u_g)/u_g$ and omitting the subscript g,

$$\begin{aligned} \alpha &= P(\eta < x \mid \eta < u^+) \\ &= \frac{P(\eta < x)}{P(\eta < u^+)} \\ &= \frac{1-\exp(-\varphi^2 x/2)}{1-\exp(-u^+\varphi^2/2)} \\ x &= \frac{-2}{\varphi^2} \log\left[1-\alpha\left\{1-\exp\left(\frac{-\varphi^2 u^+}{2}\right)\right\}\right], \end{aligned}$$

where $\alpha \sim \mathcal{U}(0,1)$.

3.9.3 *Realisations of* $\pi(\tau \mid rest)$ In order to generate from the posterior distribution of τ, we will use a similar algorithm as the one used in Section 3.9.2.

$$\begin{aligned}
\pi(\tau \mid \lambda, \gamma) &\propto \pi(\tau) \prod_{g=1}^{p} \pi(\gamma_g \mid \lambda_g, \tau) \\
&\propto \frac{1}{1+\tau^2} \prod_{g=1}^{p} \frac{1}{\lambda_g \tau} \exp\left(\frac{-\gamma_g^2}{2\lambda_g^2 \tau^2}\right) \\
&\propto \frac{1}{(1+\tau^2)\tau^p} \exp\left(\frac{-1}{2\tau^2} \sum_{g=1}^{p} \frac{\gamma_g^2}{\lambda_g^2}\right).
\end{aligned}$$

We now define the following quantities, inspired by the algorithm proposed by Scott (2011),

$$\eta = \frac{1}{\tau^2}, \quad \frac{d\tau}{d\eta} = \frac{\sqrt{\eta}}{\eta^2} \quad \varphi = \sum_{g=1}^{p} \frac{\gamma_g^2}{\lambda_g^2}.$$

We therefore obtain

$$\pi(\eta \mid \varphi) \propto \frac{1}{1+\eta} \eta^{\frac{p-1}{2}} \exp(-\eta\varphi/2).$$

The algorithm is then

- Sample $u \sim \mathcal{U}(0, 1/(1+\eta))$.
- Generate $\eta \sim \text{Gamma}\left((p+1)/2, \varphi/2\right)$, truncated to have probability 0 outside $[0, (1-u)/u]$.
- Transform back to the τ-scale, by $\tau = \sqrt{1/\eta}$.

If $F(x; a, b)$ denotes the distribution function of a Gamma distribution evaluated at x, with shape and rate parameters a and b, then sampling from a truncated Gamma is done as follows:

$$x = F^{-1}\left[\alpha F\left(u^+; \frac{p+1}{2}, \frac{\varphi}{2}\right); \frac{p+1}{2}, \frac{\varphi}{2}\right], \quad \alpha \sim \mathcal{U}(0,1), \quad u^+ = \frac{1-u}{u}.$$

3.10 *Posterior densities for the normal-gamma prior.*

3.10.1 *Realisations of* $\pi\left(\gamma_g \mid rest\right)$

$$
\begin{aligned}
\pi(\gamma_g \mid \text{rest}) &\propto \prod_{l=1}^{L} \pi(\beta_g^{(l)} \mid \gamma_g, \sigma_\beta^2)\pi(\gamma_g \mid \psi_g) \\
&\propto \exp\left\{ \frac{-\sum_{l=1}^{L}(\gamma_g - \beta_g^{(l)})^2}{2\sigma_\beta^2} - \frac{\gamma_g^2}{2\psi_g} \right\} \\
&\sim \mathcal{N}\left(\frac{\sum_{l=1}^{L} \beta_g^{(l)} \psi_g}{L\psi_g + \sigma_\beta^2}, \frac{\sigma_\beta^2 \psi_g}{L\psi_g + \sigma_\beta^2} \right).
\end{aligned}
$$

3.10.2 *Realisations of* $\pi\left(\psi_g \mid rest\right)$

$$
\begin{aligned}
\pi(\psi_g \mid \text{rest}) &\propto \pi(\psi_g \mid \lambda, \tau)\pi(\gamma_g \mid \psi_g) \\
&\propto \frac{1}{\sqrt{2\pi\psi_g}} \exp\left(\frac{-\gamma_g^2}{2\psi_g} \right) \psi_g^{\lambda-1} \exp\left(\frac{-\psi_g}{\tau} \right) \\
&\sim GIG\left(\lambda - \frac{1}{2}, \frac{1}{\tau^2}, \gamma_g^2 \right)
\end{aligned}
$$

$$
GIG(\lambda, \psi, \chi) = \frac{(\psi/\chi)^{\lambda/2}}{2K_\lambda(\sqrt{\psi\chi})} x^{\lambda-1} \exp\left\{ -\frac{1}{2}\left(\psi x + \frac{\chi}{x} \right) \right\},
$$

and K_λ is the modified Bessel function of the third kind and the parameters follow one of the conditions

$$\lambda > 0,\ \psi > 0,\ \chi \geqslant 0,$$

$$\lambda = 0,\ \psi > 0,\ \chi > 0,$$

$$\lambda < 0,\ \psi \geqslant 0,\ \chi > 0.$$

If parameters are close to zero, limiting distributions can be used (Eberlein and Hammerstein, 2004):

- if $\lambda > 0$, $\psi > 0$ but $\chi = 0$ or is close to zero, then a gamma distribution can be used instead of the generalized inverse Gaussian:

$$\text{Gamma}(\lambda, \psi/2).$$

- if $\lambda < 0$, $\chi > 0$ but $\psi = 0$ or is close to zero, then the inverse gamma distribution can be used instead of the generalized inverse Gaussian:

$$\mathrm{IG}(-\lambda, \chi/2).$$

So, using our parameters, we obtain the following cases:

- if $\lambda > 1/2$, $1/\tau^2 > 0$, $\beta_g^2 = 0$,

$$\psi_g \mid \text{rest} \sim \text{Gamma}\left(\lambda - \frac{1}{2}, \frac{1}{2\tau^2}\right).$$

- if $\lambda < 0$, $\beta_g^2 > 0$ and $1/\tau^2 = 0$, then

$$\psi_g \mid \text{rest} \sim \mathrm{IG}\left(-\lambda + \frac{1}{2}, \frac{\beta_g^2}{2}\right).$$

3.10.3 *Realisation of* $\pi(\lambda \mid \textit{rest})$

$$\begin{aligned}
\pi(\lambda \mid \text{rest}) &\propto \pi(\lambda) \prod_{g=1}^{p} \pi(\psi_g \mid \lambda) \\
&\propto e^{-\lambda} \prod_{g=1}^{p} \left(\frac{\psi_g^{\lambda-1}}{(2\tau^2)^\lambda \Gamma(\lambda)} \right) \\
&\propto e^{-\lambda} \left(\prod_{g=1}^{p} \psi_g \right)^{\lambda-1} \left[(2\tau^2)^\lambda \Gamma(\lambda)\right]^{-p}.
\end{aligned}$$

As this distribution does not have a recognizable form, we use Metropolis–Hastings step to generate from it. We put a random walk update on $\log \lambda$ leading to the proposal

$$\lambda' = \exp\{\sigma_\lambda^2 z\}\lambda,$$

where z is generated from a standard normal distribution, and σ_λ is chosen so that the overall acceptance probability is about 30% in average. The corresponding τ' can be taken to be $\tau' = \sqrt{2\lambda\tau^2/(2\lambda')}$. Then the acceptance probability is

$$\alpha = \min\left[1, e^{-\lambda'+\lambda}\left(\prod_{g=1}^{p}\psi\right)^{\lambda'-\lambda}\left(\frac{\Gamma(\lambda)}{\Gamma(\lambda')}\right)^{p}\frac{(2\tau^2)^{p\lambda}}{(2\tau'^2)^{p\lambda'}}\frac{\lambda'}{\lambda}\exp\left\{\sum_{g=1}^{p}\psi_g\left(\frac{1}{2\tau^2}-\frac{1}{2\tau^2}\right)\right\}\right]$$

$$\begin{aligned}\log(\alpha) =& (\lambda'-\lambda)\left[-1+\sum_{g=1}^{p}\log\psi_g\right]+(\log\lambda'-\log\lambda)+p(\log\Gamma(\lambda)-\log\Gamma(\lambda'))\\ &+p\lambda\log(2\tau^2)-\lambda' p\log(2\tau'^2)+\sum_{g=1}^{p}\psi_g\left(\frac{1}{2\tau^2}-\frac{1}{2\tau'^2}\right).\end{aligned}$$

3.10.4 *Realisation of* $\pi(\tau^2 \mid rest)$

$$\begin{aligned}\pi(\tau^{-2}\mid \text{rest}) &\propto \prod_{g=1}^{p}\pi(\psi_g\mid\lambda,\tau^{-2})\pi(\tau^{-2})\\ &\propto \tau^{-2}\exp\left\{-\frac{\tau^{-2}M}{2\lambda}\right\}\prod_{g=1}^{p}\left(\frac{\tau^{-2}}{2}\right)^{\lambda}\exp\left\{-\frac{\psi_g\tau^{-2}}{2}\right\}\\ &\propto \left(\tau^{-2}\right)^{2+\lambda p-1}\exp\left\{-\tau^{-2}\left(\frac{M}{2\lambda}+\sum_{g=1}^{p}\frac{\psi_g}{2}\right)\right\}\\ &\sim \text{Gamma}\left(2+\lambda p, \frac{M}{2\lambda}+\sum_{g=1}^{p}\frac{\psi_g}{2}\right).\end{aligned}$$

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